

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd

OM protein - protein search, using swi model

Run on: June 25, 2003, 14:38:41 ; Search time 27.1047 Seconds
(without alignments)
843.812 Million cell updates/sec

Title: US-09-622-613B-21

Sequence: 1 MQNWATFQOKHINTPICN.....ICVKCENQYPVHFAGIGRCP 111

Scoring table: BLJDSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

```
Minimum DB seq length: 0
Maximum DB seq length: 200000000000
```

Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SPTREMBL_21:*

- 1: sp.archaea:*
- 2: sp.bacteria:*
- 3: sp.fungi:*
- 4: sp.human:*
- 5: sp.invertebrate:*
- 6: sp.mammal:*
- 7: sp.mmc:*
- 8: sp.organelle:*
- 9: sp.phage:*
- 10: sp.plant:*
- 11: sp.podent:*
- 12: sp.virus:*
- 13: sp.vertebrate:*
- 14: sp.unclassified:*
- 15: sp.virus:*
- 16: sp.bacterioph:*
- 17: sp.archaeap:*

Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	585.5	96.8	133	13	Q9PWR7	Q9PWR7 rana cates
2	554.5	91.7	133	13	Q98SM0	Q98SM0 rana cates
3	483.5	79.9	132	13	Q98SM2	Q98SM2 rana cates
4	474.5	78.4	133	13	Q98SL9	Q98SL9 rana cates
5	467.5	77.3	133	13	Q98SL8	Q98SL8 rana cates
6	444.5	73.5	132	13	Q98SM1	Q98SM1 rana cates
7	372	61.5	132	13	Q9DPF78	Q9DPF78 rana cates
8	277.5	45.9	127	13	Q918V8	Q918V8 rana pipie
9	273.5	45.2	127	13	Q8UVX5	Q8UVX5 rana pipie
10	243	40.2	129	13	Q9DPFV6	Q9DPFV6 rana cates
11	225.5	37.3	128	13	Q9DPFV8	Q9DPFV8 rana cates
12	223.5	36.9	128	13	Q9DFV7	Q9DFV7 rana cates
13	214.5	35.5	128	13	Q9DPFV5	Q9DPFV5 rana cates
14	161	26.6	169	13	Q9W738	Q9W738 xenopus la
15	128	21.2	170	6	Q9BECl	Q9BECl tragus ja
16	123.5	20.1	116	6	Q9TVC0	Q9TVC0 sus scrofa

ALIGNMENTS

17	121.5	20.1	163	6	09BDC2	09bdc2 antilocapra
18	121	20.0	150	11	08V994	08v994 beryllmys bo
19	119	19.7	150	11	08V988	08v988 rattus norv
20	118.5	19.6	144	6	09BH14	09bh14 antilocapra
21	116	19.2	150	11	08VD92	08vd92 rattus exul
22	113.5	18.8	152	11	08V989	08v89 rattus norv
23	112.5	18.6	119	6	09TV33	09tv33 bos taurus
24	110.5	18.3	124	6	095N66	095ne6 bubalus bub
25	109.5	18.1	149	11	08V995	08vd95 beryllmys bo
26	109	18.0	124	6	09BEC2	09bec2 rattus norv
27	109	18.0	134	6	09BDB9	09bdb9 rattus ja
28	108.5	17.9	152	11	08VB84	08vbd4 rattus lion
29	108.5	17.9	156	6	08S005	08sq05 lagotherix l
30	107.5	17.8	119	6	09TV30	09tv30 sequinus oe
31	107.5	17.8	119	6	09TV28	09tv28 eulemur ful
32	106.5	17.6	124	6	09TV82	09tv82 bos taurus
33	106.5	17.6	156	6	08S006	08sq06 ateles geof
34	105.5	17.4	142	6	09BEC3	09bec3 rattus ja
35	105.5	17.4	156	6	08S008	08sq08 saimiri sci
36	105.5	17.4	156	6	08S007	08sq07 sequinus oe
37	104.5	17.3	152	11	08V990	08v990 rattus fusc
38	103.5	17.1	116	6	097933	097933 phocoenoid
39	103.5	17.1	149	11	08V993	08v993 rattus exul
40	102.5	16.9	116	6	097934	097934 pseudorca c
41	102.5	16.9	119	6	09TS06	09ts06 ceropithec
42	101.5	16.8	119	6	09TV32	09tv32 gorilla gor
43	101.5	16.8	124	6	09XS40	09xs40 camelus bac
44	101.5	16.8	157	11	09JXJ4	09jxj4 meriones un
45	101.5	16.8	158	6	08SP73	08sp73 sequinus la

RESULT 1

ID	OSPMWT;	PRELIMINARY;	PRT;	133 AA.
AC	09PMW7;			
DT	01-MAY-2000 (TrEMBLrel. 13, Created)			
DT	01-MAY-2000 (TrEMBLrel. 13, last sequence update)			
DT	01-DEC-2001 (TrEMBLrel. 19, last annotation update)			
DE	Ribonuclease precursor.			
GN	RCR.			
OS	Rana catesbeiana (Bull frog).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae; Rana.			
OX	NCBI_TaxID=8400;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=LIVER;			
RX	MEDLINE=98165825; PubMed=9497370;			
RA	Huang H.C., Wang S.C., Leu Y.J., Lu S.C., Liao Y.D.;			
RT	"The Rana catesbeiana rcr gene encoding a cytotoxic ribonuclease.			
RT	Tissue distribution, cloning, purification, cytotoxicity, and active			
RT	residues for RNase activity.";			
RL	J. Biol. Chem. 273:6395-6401(1998).			
DR	EMBL: AF039104; AAD10702.1; -			
DR	HSP: P11916; IBC4.			
DR	InterPro: IPR001427; RNaseA.			
DR	Pfam: PF00074; .rnasea; 1.			
DR	ProDom: PD000535; RNaseA; 1.			
DR	SMART: SM00092; RNase_Pc; 1.			
DR	PROSITE: PS00127; RNASE_PANCREATIC; UNKNOWN_1.			
FW	Signal.			
FT	SIGNAL	1	22	POTENTIAL.
FT	CHAIN	23	133	RIBONUCLEASE.
SO	SEQUENCE	133 AA; 14762 MW; A7062594F7D16F0C CRC64;		
Query Match		96.8%;	Score 585.5; DB 13;	Length 133;
Best Local Similarity		97.3%;	Pred. No. 6; 6e-60;	
Matches 108; Conservative		2; Mismatches 0; Indels 1; Gaps 1		

```

Db      23 QNMATFOOKHINTPII-CNTILDNNIYVGGCKRVNFTFISSATVKAICTGVINLV 82
Oy      61 LSTRFOLNCTRTSTIPRCPYSSRTETNYICVKCENQPVHFGIGRCP 111
Db      83 LSTRFOLNCTRTSTIPRCPYSSRTETNYICVKCENQPVHFGIGRCP 133

```

RESULT 2

```

O98SMO ID Q98SMO PRELIMINARY: PRT: 133 AA.

```

```

AC Q98SMO: 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DE 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE RNase A-type ribonuclease rc208 precursor.
OS Rana catesbeiana (Bull frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Rana.
OX NCBI_TaxID=8400;

```

```

RP SEQUENCE FROM N.A.
RX MEDLINE=21539506; PubMed=11683320;
RA Rosenberg H.F., Zhang J., Liao Y.-D., Dyer K.D.;
RT "Rapid diversification of RNase A superfamily ribonuclease from the
RT bullfrog, Rana catesbeiana."
RL J. Mol. Evol. 53:31-38(2001).
DR EMBL: AF351209; AAK30255.1; -.
DR HSSP: P11916; IBC4.
DR InterPro: IPR001427; RNaseA.
DR Pfam: PF00074; rnasea: 1.
DR ProDom: PD000535; RNaseA: 1.
DR SMART: SM00092; RNase_Pc: 1.
DR PROSITE: PS00127; RNASE_PANCREATIC; UNKNOWN_1.
KW Signal.
FT SIGNAL.
SQ SEQUENCE 133 AA: 14628 MW: 8785B236B26E54E CRC64:

```

```

Query Match          91.7%; Score 554.5; DB 13; Length 133;
Best Local Similarity 92.8%; Pred. No. 2.5e-56;
Matches 103; Conservative 2; Mismatches 5; Indels 1; Gaps 1;

```

```

Oy      2 QNMATFOOKHINTPII-CNTILDNNIYVGGCKRVNFTFISSATVKAICTGVINLV 60
Db      23 QNMATFOOKHINTPII-CNTILDNNIYVGGCKRVNFTFISSATVKAICTGVINLV 82
Oy      61 LSTRFOLNCTRTSTIPRCPYSSRTETNYICVKCENQPVHFGIGRCP 111
Db      83 LSTRFOLNCTRTSTIPRCPYSSRTETNYICVKCENQPVHFGIGRCP 133

```

RESULT 3

```

O98SM2 ID Q98SM2 PRELIMINARY: PRT: 132 AA.

```

```

AC Q98SM2: 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DE 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE RNase A-type ribonuclease rc203 precursor (RC-RNase7 precursor).
OS Rana catesbeiana (Bull frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Rana.
OX NCBI_TaxID=8400;

```

```

RP SEQUENCE FROM N.A.
RX MEDLINE=21539506; PubMed=11683320;
RA Rosenberg H.F., Zhang J., Liao Y.-D., Dyer K.D.;
RT "Rapid diversification of RNase A superfamily ribonuclease from the
RT bullfrog, Rana catesbeiana."
RL J. Mol. Evol. 53:31-38(2001).

```

```

RP SEQUENCE FROM N.A.
RC TISSUE=LIVER;

```

```

RA Liao Y.-D., Tang P.-C., Jeng J.-T.;
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF351207; AAK30253.1; -.
DR EMBL: AF359578; AAL87036.1; -.
DR HSSP: P11916; IBC4.
DR InterPro: IPR001427; RNaseA.
DR Pfam: PF00074; rnasea: 1.
DR ProDom: PD000535; RNaseA: 1.
DR SMART: SM00092; RNase_Pc: 1.
DR PROSITE: PS00127; RNASE_PANCREATIC; UNKNOWN_1.
KW Signal.
FT SIGNAL.
FT CHAIN 23 132 RC-RNase7.
SQ SEQUENCE 132 AA: 14412 MW: 131A745187978687 CRC64:

```

```

Query Match          79.9%; Score 483.5; DB 13; Length 132;
Best Local Similarity 82.7%; Pred. No. 3.9e-48;
Matches 91; Conservative 6; Mismatches 12; Indels 1; Gaps 1;

```

```

Oy      2 QNMATFOOKHINTPII-CNTILDNNIYVGGCKRVNFTFISSATVKAICTGVINLV 60
Db      23 QNMATFOOKHINTPII-CNTILDNNIYVGGCKRVNFTFISSATVKAICTGVINLV 82
Oy      61 LSTRFOLNCTRTSTIPRCPYSSRTETNYICVKCENQPVHFGIGRCP 110
Db      83 LSTRFOLNCTRTSTIPRCPYSSRTETNYICVKCENQPVHFGIGRCP 132

```

RESULT 4

```

O98SL9 ID Q98SL9 PRELIMINARY: PRT: 133 AA.

```

```

AC Q98SL9: 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DE 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE RNase A-type ribonuclease rc212 precursor.
OS Rana catesbeiana (Bull frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Rana.
OX NCBI_TaxID=8400;

```

```

RP SEQUENCE FROM N.A.
RX MEDLINE=21539506; PubMed=11683320;
RA Rosenberg H.F., Zhang J., Liao Y.-D., Dyer K.D.;
RT "Rapid diversification of RNase A superfamily ribonuclease from the
RT bullfrog, Rana catesbeiana."
RL J. Mol. Evol. 53:31-38(2001).
DR EMBL: AF351210; AAK30256.1; -.
DR HSSP: P11916; IBC4.
DR InterPro: IPR001427; RNaseA.
DR Pfam: PF00074; rnasea: 1.
DR ProDom: PD000535; RNaseA: 1.
DR SMART: SM00092; RNase_Pc: 1.
DR PROSITE: PS00127; RNASE_PANCREATIC; UNKNOWN_1.
KW Signal.
FT SIGNAL.
FT CHAIN 1 22 POTENTIAL.
SQ SEQUENCE 133 AA: 14615 MW: C8785B236B26E54E CRC64:

```

```

Query Match          78.4%; Score 474.5; DB 13; Length 133;
Best Local Similarity 77.5%; Pred. No. 4.3e-47;
Matches 86; Conservative 12; Mismatches 12; Indels 1; Gaps 1;

```

```

Oy      2 QNMATFOOKHINTPII-CNTILDNNIYVGGCKRVNFTFISSATVKAICTGVINLV 60
Db      23 QNMATFOOKHINTPII-CNTILDNNIYVGGCKRVNFTFISSATVKAICTGVINLV 82
Oy      61 LSTRFOLNCTRTSTIPRCPYSSRTETNYICVKCENQPVHFGIGRCP 111
Db      83 LSTRFOLNCTRTSTIPRCPYSSRTETNYICVKCENQPVHFGIGRCP 133

```

RESULT 5

```

O98SL8

```

ID 098SL8 PRELIMINARY; PRT; 133 AA.
AC 098SL8;
DT 01-JUN-2001 (TREMblrel. 17, Created)
DT 01-JUN-2001 (TREMblrel. 17, Last sequence update)
DE 01-DEC-2001 (TREMblrel. 19, Last annotation update)
OS Rana catesbeiana (bull frog).
OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.
NCBI_TaxID=8400;
RN [1]
RP MEDLINE-21539506; PubMed-11683320;
RA Rosenberg H.F., Zhang J., Liao Y.-D., Dyer K.D.;
RT "Rapid diversification of RNase A superfamily ribonuclease from the
RT bullfrog, *Rana catesbeiana*.";
RL J. Mol. Evol. 53:31-38(2001).
DR EMBL; AF51211; AAC30257.1; -;
DR HSSP; P11916; IBC4.
DR InterPro: IPR001427; RNaseA.
DR Pfam: PF00074; RNaseA; 1.
DR ProDom: PD000535; RNaseA; 1.
DR SMART; SM00092; RNase_PC; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; UNKNOWN_1.
KW Signal.
FT SIGNAL.
SQ SEQUENCE 133 AA; 14590 MW; 8B40B9A94FA5B943 CRC64;
POTENTIAL.
Query Match 77.3%; Score 467.5; DB 13; Length 133;
Best Local Similarity 75.7%; Pred. No. 2.8e-46;
Matches 84; Conservative 14; Mismatches 12; Indels 1; Gaps 1;
ID 098SM1 PRELIMINARY; PRT; 132 AA.
AC 098SM1;
DT 01-JUN-2001 (TREMblrel. 17, Created)
DT 01-JUN-2001 (TREMblrel. 17, Last sequence update)
DE 01-DEC-2001 (TREMblrel. 19, Last annotation update)
OS Rana catesbeiana (bull frog).
OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.
NCBI_TaxID=8400;
RN [1]
RP MEDLINE-21539506; PubMed-11683320;
RA Rosenberg H.F., Zhang J., Liao Y.-D., Dyer K.D.;
RT "Rapid diversification of RNase A superfamily ribonuclease from the
RT bullfrog, *Rana catesbeiana*.";
RL J. Mol. Evol. 53:31-38(2001).
DR EMBL; AF51208; AAC30254.1; -;
DR HSSP; P11916; IBC4.
DR InterPro: IPR001427; RNaseA.
DR Pfam: PF00074; RNaseA; 1.
DR ProDom: PD000535; RNaseA; 1.
DR SMART; SM00092; RNase_PC; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; UNKNOWN_1.
KW Signal.
FT SIGNAL.
SQ SEQUENCE 132 AA; 14704 MW; 95D61760F729868E CRC64;
POTENTIAL.
Query Match 73.5%; Score 444.5; DB 13; Length 132;
Best Local Similarity 77.3%; Pred. No. 1.2e-43;

Matches 85; Conservative 8; Mismatches 16; Indels 1; Gaps 1;
ID 09DF78 PRELIMINARY; PRT; 132 AA.
AC 09DF78;
DT 01-MAR-2001 (TREMblrel. 16, Created)
DT 01-OCT-2001 (TREMblrel. 18, Last sequence update)
DE 01-DEC-2001 (TREMblrel. 19, Last annotation update)
OS Rana catesbeiana (bull frog).
OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.
NCBI_TaxID=8400;
RN [1]
RP MEDLINE-20512555; PubMed-11058105;
RA Liao Y.-D., Huang H.-C., Leu Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.;
RT "Purification and cloning of cytoxic ribonucleases from *Rana*
RT catesbeiana (bullfrog).";
RL Nucleic Acids Res. 28:4097-4104(2000).
RN [2]
RP TISSUE=LIVER.
RA Liao Y.-D., Huang H.-C., Leu Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.;
RL Submitted (AUG-2001) to the EMBL/Genbank/DBJ databases.
DR EMBL; AF288642; AAC30414.2; -;
DR HSSP; P11916; IBC4.
DR InterPro: IPR001427; RNaseA.
DR Pfam: PF00074; RNaseA; 1.
DR ProDom: PD000535; RNaseA; 1.
DR SMART; SM00092; RNase_PC; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; UNKNOWN_1.
KW Signal.
FT SIGNAL.
SQ SEQUENCE 132 AA; 14625 MW; DBD9A517452FBE53 CRC64;
POTENTIAL.
Query Match 61.5%; Score 372; DB 13; Length 132;
Best Local Similarity 64.9%; Pred. No. 2.9e-35;
Matches 72; Conservative 10; Mismatches 27; Indels 2; Gaps 2;
ID 0918V8 PRELIMINARY; PRT; 127 AA.
AC 0918V8;
DT 01-OCT-2000 (TREMblrel. 15, Created)
DT 01-OCT-2000 (TREMblrel. 15, Last sequence update)
DE 01-DEC-2001 (TREMblrel. 19, Last annotation update)
OS Onconase variant rap1 precursor.
OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.
NCBI_TaxID=8404;
RN [1]
RP MEDLINE-20512555; PubMed-11058105;
RA Liao Y.-D., Huang H.-C., Leu Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.;
RT "Purification and cloning of cytoxic ribonucleases from *Rana*
RT catesbeiana (bullfrog).";
RL Nucleic Acids Res. 28:4097-4104(2000).
RN [2]
RP TISSUE=LIVER.
RA Liao Y.-D., Huang H.-C., Leu Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.;
RL Submitted (AUG-2001) to the EMBL/Genbank/DBJ databases.
DR EMBL; AF288642; AAC30414.2; -;
DR HSSP; P11916; IBC4.
DR InterPro: IPR001427; RNaseA.
DR Pfam: PF00074; RNaseA; 1.
DR ProDom: PD000535; RNaseA; 1.
DR SMART; SM00092; RNase_PC; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; UNKNOWN_1.
KW Signal.
FT SIGNAL.
SQ SEQUENCE 132 AA; 14625 MW; DBD9A517452FBE53 CRC64;
POTENTIAL.
Query Match 61.5%; Score 372; DB 13; Length 132;
Best Local Similarity 64.9%; Pred. No. 2.9e-35;
Matches 72; Conservative 10; Mismatches 27; Indels 2; Gaps 2;
ID 0918V8 PRELIMINARY; PRT; 127 AA.
AC 0918V8;
DT 01-OCT-2000 (TREMblrel. 15, Created)
DT 01-OCT-2000 (TREMblrel. 15, Last sequence update)
DE 01-DEC-2001 (TREMblrel. 19, Last annotation update)
OS Onconase variant rap1 precursor.
OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.
NCBI_TaxID=8404;
RN [1]
RP MEDLINE-20512555; PubMed-11058105;
RA Liao Y.-D., Huang H.-C., Leu Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.;
RT "Purification and cloning of cytoxic ribonucleases from *Rana*
RT catesbeiana (bullfrog).";
RL Nucleic Acids Res. 28:4097-4104(2000).
RN [2]
RP TISSUE=LIVER.
RA Liao Y.-D., Huang H.-C., Leu Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.;
RL Submitted (AUG-2001) to the EMBL/Genbank/DBJ databases.
DR EMBL; AF288642; AAC30414.2; -;
DR HSSP; P11916; IBC4.
DR InterPro: IPR001427; RNaseA.
DR Pfam: PF00074; RNaseA; 1.
DR ProDom: PD000535; RNaseA; 1.
DR SMART; SM00092; RNase_PC; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; UNKNOWN_1.
KW Signal.
FT SIGNAL.
SQ SEQUENCE 132 AA; 14625 MW; DBD9A517452FBE53 CRC64;
POTENTIAL.
Query Match 61.5%; Score 372; DB 13; Length 132;
Best Local Similarity 64.9%; Pred. No. 2.9e-35;
Matches 72; Conservative 10; Mismatches 27; Indels 2; Gaps 2;

RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=LIVER.
 RX MEDLINE=20330357; PubMed=10871370;
 RA Chen S.-L., Le S.-Y., Newton D.L., Maizel J.V. Jr., Rybak S.M.;
 RT "A gender-specific mRNA encoding a cytotoxic ribonuclease contains a
 3 UTR of unusual length and structure."
 RL Nucleic Acids Res. 28:2375-2382(2000).
 DR EMBL: AF165133; AAF76935.1; -
 DR HSSP: P22069; 10NC.
 DR InterPro: IPR001427; RNaseA.
 DR Pfam: PF00074; rnaasea; 1.
 DR ProDom: PD000535; RNaseA; 1.
 DR SMART: SM00092; RNase_Pc; 1.
 DR PROSITE: PS00127; RNASE_PANCREATIC; UNKNOWN_1.
 KW Signal.
 FT SIGNAL.
 SQ SEQUENCE 127 AA; 14491 MW; B8511DC5407AB69B CRC64;

Query Match 45.9%; Score 277.5; DB 13; Length 127;
 Best Local Similarity 48.6%; Pred. No. 2.3e-24;
 Matches 54; Conservative 16; Mismatches 32; Indels 9; Gaps 4;

QY 2 ONMATEFOQKHIIINT-PIICNTILDNNIYVGGCKRVNTFIISATTVKAICTGVI-NLN 59
 DB 24 QDMLEFQKHLNTRDVCNINIMSTLNF---HCKDKNTFTYSRPEPVKAICKGIIASKN 79
 QY 60 VLSTTRFQNLCTRTSITPRCPYSSRTETNYICVKCENQYVPHFAGICRC 110
 DB 80 VLTSEFYLSDC---NVTSRPKYKLLKSTNFCVTCENQAPVHFVGVC 127

RESULT 9
 Q8UVX5 PRELIMINARY; PRT: 127 AA.
 AC Q8UVX5:
 DT 01-MAR-2002 (TREMBLrel. 20, Created)
 DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE Oncocase precursor.
 GN RPR.
 OS Rana pipiens (Northern leopard frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae; Rana.
 OX NCBI_TaxID=8404;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Liao Y.-D., Wang S.-C.;
 RT Submitted (DEC-2000) to the EMBL/Genbank/DBJ databases.
 RL EMBL: AF332139; AAL54383.1; -
 DR InterPro: IPR001427; RNaseA.
 DR Pfam: PF00074; rnaasea; 1.
 DR ProDom: PD000535; RNaseA; 1.
 DR SMART: SM00092; RNase_Pc; 1.
 DR PROSITE: PS00127; RNASE_PANCREATIC; UNKNOWN_1.
 KW Signal.
 FT SIGNAL.
 SQ SEQUENCE 127 AA; 14469 MW; 953F90D351CFEEF3 CRC64;

Query Match 45.2%; Score 273.5; DB 13; Length 127;
 Best Local Similarity 48.6%; Pred. No. 6.6e-24;
 Matches 54; Conservative 16; Mismatches 32; Indels 9; Gaps 4;

QY 2 ONMATEFOQKHIIINT-PIICNTILDNNIYVGGCKRVNTFIISATTVKAICTGVI-NLN 59
 DB 24 QDMLEFQKHLNTRDVCNINIMSTLNF---HCKDKNTFTYSRPEPVKAICKGIIASKN 79
 QY 60 VLSTTRFQNLCTRTSITPRCPYSSRTETNYICVKCENQYVPHFAGICRC 110
 DB 80 VLTSEFYLSDC---NVTSRPKYKLLKSTNFCVTCENQAPVHFVGVC 127

RESULT 10
 Q9DFY6 PRELIMINARY; PRT: 129 AA.
 AC Q9DFY6:
 DT 01-MAR-2001 (TREMBLrel. 16, Created)
 DT 01-OCT-2001 (TREMBLrel. 18, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE RC-RNase2 ribonuclease precursor.
 OS Rana catesbeiana (Bull frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae; Rana.
 OX NCBI_TaxID=8400;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=LIVER.
 RX MEDLINE=20512555; PubMed=11058105;
 RA Liao Y.D., Huang H.C., Leu Y.-J., Wei C.W., Tang P.C., Wang S.C.;
 RT "Purification and cloning of cytotoxic ribonucleases from Rana
 catesbeiana (bullfrog)."
 RL Nucleic Acids Res. 28:4097-4104(2000).
 DR EMBL: AF242555; AAG31441.2; -
 DR HSSP: P22069; 10NC.
 DR InterPro: IPR001427; RNaseA.
 DR Pfam: PF00074; rnaasea; 1.
 DR ProDom: PD000535; RNaseA; 1.
 DR SMART: SM00092; RNase_Pc; 1.
 DR PROSITE: PS00127; RNASE_PANCREATIC; UNKNOWN_1.
 KW Signal.
 FT CHAIN.
 SQ SEQUENCE 129 AA; 14724 MW; 826A62882B10ABDA CRC64;

Query Match 40.2%; Score 243; DB 13; Length 129;
 Best Local Similarity 42.5%; Pred. No. 2.2e-20;
 Matches 48; Conservative 25; Mismatches 30; Indels 10; Gaps 5;

QY 2 ONMATEFOQKHIIINT-PIICNTILDNNIYVGGCKRVNTFIISATTVKAICTGVI-NLN 59
 DB 24 QDMATEFKKHLNTRDVCNINIMPTSLF---DCKDKNTFTYSLPGPVKAICKGVIIFSAD 79
 QY 60 VLSTTRFQNLCTRTSITPR-PCPYSSRTETNYICVKCENQYVPHFAGICRCP 111
 DB 80 VLSNSEFYLAEC---NVKPRPKYKLLKSSNRICICEHLPVHFAGVIGCP 129

RESULT 11
 Q9DFY8 PRELIMINARY; PRT: 128 AA.
 AC Q9DFY8:
 DT 01-MAR-2001 (TREMBLrel. 16, Created)
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE RC-RNase2 ribonuclease precursor.
 OS Rana catesbeiana (Bull frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae; Rana.
 OX NCBI_TaxID=8400;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=LIVER.
 RX MEDLINE=20512555; PubMed=11058105;
 RA Liao Y.D., Huang H.C., Leu Y.-J., Wei C.W., Tang P.C., Wang S.C.;
 RT "Purification and cloning of cytotoxic ribonucleases from Rana
 catesbeiana (bullfrog)."
 RL Nucleic Acids Res. 28:4097-4104(2000).
 DR EMBL: AF242555; AAG31441.2; -
 DR HSSP: P22069; 10NC.
 DR InterPro: IPR001427; RNaseA.
 DR Pfam: PF00074; rnaasea; 1.
 DR ProDom: PD000535; RNaseA; 1.
 DR SMART: SM00092; RNase_Pc; 1.
 DR PROSITE: PS00127; RNASE_PANCREATIC; UNKNOWN_1.
 KW Signal.
 FT CHAIN.
 SQ SEQUENCE 128 AA; 14724 MW; 826A62882B10ABDA CRC64;

RA Liao Y.-D., Huang H.-C., Leu Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.;
 RL Submitted (Aug-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF242553; AAC31439.1;
 DR HSSP: P22069; 10NC;
 DR InterPro: IPR001427; RNaseA.
 DR Pfam: PF00074; RNaseA; 1.
 DR ProDom: PD000535; RNaseA; 1.
 DR SMART: SM00092; RNase_Pc; 1.
 DR PROSITE: PS00127; RNase_PANCREATIC; UNKNOWN_1.
 KW Signal.
 FT SIGNAL.
 FT CHAIN 1 23 POTENTIAL.
 FT CHAIN 24 128 RC-RNASE3 RIBONUCLEASE.
 SQ SEQUENCE 128 AA; 14839 MW; 989719CF52053ECC CRC64;

Query Match 37.3%; Score 225.5; DB 13; Length 128;
 Best Local Similarity 39.3%; Pred. No. 2.3e-18;
 Matches 44; Conservative 21; Mismatches 98; Indels 9; Gaps 4;

OY 2 QNATFOCKHILNT-PIICNTILDNNIYVGCGCKRVNFTIISATVKAICTGV-INLN 59
 DB 24 QNMTFOCKHILTDTRVQCAEMKALF---DCKKNTFIYARPGVQALCKNIYSKN 79
 60 VLSTRRLNCTRTSTIPRCPPSSRTETNYICVCKENQPVHFAIGRCP 111
 80 VLSTEEFYLDQCNRIKL---PCHYKTKKSSNTICITCENKLPVHFAVEECP 128

RESULT 12

O9DFY7 PRELIMINARY; PRT; 128 AA.
 AC Q9DFY7;
 DT 01-MAR-2001 (TREMBLrel. 16, Created)
 DT 01-OCT-2001 (TREMBLrel. 18, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE RC-RNase3 ribonuclease precursor.
 OS Rana catesbeiana (Bull frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranidae; Ranidae; Rana.
 OX NCBI_Taxid=8400;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=LIVER;
 RX MEDLINE=20512555; PubMed=11058105;
 RA Liao Y.-D., Huang H.-C., Leu Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.;
 RT "Purification and cloning of cytotoxic ribonucleases from Rana
 catesbeiana (bullfrog)."
 RL Nucleic Acids Res. 28:4097-4104(2000).
 DR EMBL: AF242554; AAC31440.2;
 DR HSSP: P22069; 10NC;
 DR InterPro: IPR001427; RNaseA.
 DR Pfam: PF00074; RNaseA; 1.
 DR ProDom: PD000535; RNaseA; 1.
 DR SMART: SM00092; RNase_Pc; 1.
 DR PROSITE: PS00127; RNase_PANCREATIC; UNKNOWN_1.
 KW Signal.
 FT SIGNAL.
 FT CHAIN 1 23 POTENTIAL.
 FT CHAIN 24 128 RC-RNASE3 RIBONUCLEASE.
 SQ SEQUENCE 128 AA; 14517 MW; 2B14986082E0587D CRC64;

Query Match 36.9%; Score 223.5; DB 13; Length 128;
 Best Local Similarity 40.2%; Pred. No. 4e-18;
 Matches 45; Conservative 19; Mismatches 39; Indels 9; Gaps 4;

OY 2 QNATFOCKHILNT-PIICNTILDNNIYVGCGCKRVNFTIISATVKAICTGV-INLN 59
 DB 24 QDMTFPOCKHILTDTRVQCAEMKALF---DCKKNTFIYALPGRVQALCKNIIRNTD 79
 60 VLSTRRLNCTRTSTIPRCPPSSRTETNYICVCKENQPVHFAIGRCP 111
 80 VLSDNALDQCNRIKL---PCHYKTKKSSNTICITCENKLPVHFAVGSCP 128

RESULT 13

O9DFY5 PRELIMINARY; PRT; 128 AA.
 AC O9DFY5;
 DT 01-MAR-2001 (TREMBLrel. 16, Created)
 DT 01-OCT-2001 (TREMBLrel. 18, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE RC-RNase6 ribonuclease precursor.
 OS Rana catesbeiana (Bull frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranidae; Ranidae; Rana.
 OX NCBI_Taxid=8400;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=LIVER;
 RX MEDLINE=20512555; PubMed=11058105;
 RA Liao Y.-D., Huang H.-C., Leu Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.;
 RT "Purification and cloning of cytotoxic ribonucleases from Rana
 catesbeiana (bullfrog)."
 RL Nucleic Acids Res. 28:4097-4104(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=LIVER;
 RA Liao Y.-D., Huang H.-C., Leu Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.;
 RL Submitted (Aug-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF242556; AAC31442.2;
 DR HSSP: P22069; 10NC;
 DR InterPro: IPR001427; RNaseA.
 DR Pfam: PF00074; RNaseA; 1.
 DR ProDom: PD000535; RNaseA; 1.
 DR SMART: SM00092; RNase_Pc; 1.
 DR PROSITE: PS00127; RNase_PANCREATIC; UNKNOWN_1.
 KW Signal.
 FT SIGNAL.
 FT CHAIN 1 23 POTENTIAL.
 FT CHAIN 24 128 RC-RNASE6 RIBONUCLEASE.
 SQ SEQUENCE 128 AA; 14804 MW; AFE6FD67D266C7C2 CRC64;

Query Match 35.5%; Score 214.5; DB 13; Length 128;
 Best Local Similarity 38.4%; Pred. No. 4.3e-17;
 Matches 43; Conservative 20; Mismatches 40; Indels 9; Gaps 4;

OY 2 QNATFOCKHILNT-PIICNTILDNNIYVGCGCKRVNFTIISATVKAICTGV-INLN 59
 DB 24 QDMTFPOCKHILTDTRVQCAEMKALF---DCKKNTFIYARPGVQALCKNIYKNTN 79
 60 VLSTRRLNCTRTSTIPRCPPSSRTETNYICVCKENQPVHFAIGRCP 111
 80 VLSDVEFYLDQCNRIKL---PCHYRLDGSNTICITCENKLPVHFAVGRCP 128

RESULT 14

O9W738 PRELIMINARY; PRT; 169 AA.
 AC O9W738;
 DT 01-NOV-1999 (TREMBLrel. 12, Created)
 DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE FRU2 protein.
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipridae; Pipridae;
 OC Xenopodinae; Xenopus.
 OX NCBI_Taxid=8355;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC MEDLINE=96069863; PubMed=7585965;
 RA Kinoshita N., Minshull J., Kirschner M.W.;
 RT "The identification of two novel ligands of the fgr receptor by a
 yeast screening method and their activity in Xenopus development."
 RL Cell 83:621-630(1995).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Kinoshita N., Kirschner M.W.;

